

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/986,682A

2/04

DATE: 02/21/2002  
TIME: 22:54:14

INPUT SET: S36770.raw

#4

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

- 1
- 2
- 3 (1) General Information:
- 4 (i) APPLICANT: Tsusaki et al.
- 5 (ii) TITLE OF INVENTION: POLYPEPTIDE HAVING -FRUCTOFURANOSIDASE
- 6 ACTIVITY
- 7 (iii) NUMBER OF SEQUENCES: 6
- 8 (iv) CORRESPONDENCE ADDRESS:
- 9 (A) ADDRESSEE: BROWDY AND NEIMARK
- 10 (B) STREET: 419 Seventh Street, N.W., Suite 300
- 11 (C) CITY: Washington
- 12 (D) STATE: D.C.
- 13 (E) COUNTRY: USA
- 14 (F) ZIP: 20004
- 15 (v) COMPUTER READABLE FORM:
- 16 (A) MEDIUM TYPE: Floppy disk
- 17 (B) COMPUTER: IBM PC compatible
- 18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 19 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 20 (vi) CURRENT APPLICATION DATA:
- 21 (A) APPLICATION NUMBER: 09/986,682
- 22 (B) FILING DATE:
- 23 (C) CLASSIFICATION:
- 24 (vii) PRIOR APPLICATION DATA:
- 25 (A) APPLICATION NUMBER: US/09/317,179
- 26 (B) FILING DATE:
- 27 (viii) ATTORNEY/AGENT INFORMATION:
- 28 (A) NAME: BROWDY, Roger L.
- 29 (B) REGISTRATION NUMBER: 25,618
- 30 (C) REFERENCE/DOCKET NUMBER: TSUSAKI=2
- 31 (ix) TELECOMMUNICATION INFORMATION:
- 32 (A) TELEPHONE: 202-628-5197
- 33 (B) TELEFAX: 202-737-3528
- 34 (2) INFORMATION FOR SEQ ID NO: 1:
- 35 (i) SEQUENCE CHARACTERISTICS:
- 36 (A) LENGTH: 21 amino acids
- 37 (B) TYPE: amino acid
- 38 (D) TOPOLOGY: linear
- 39 (v) FRAGMENT TYPE: N-terminal fragment
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
- 41 Met Asn Ser Gly Asp Tyr Lys Glu Asp Tyr Gly Phe Ala His Ile Thr
- 42 1 5 10 15
- 43 Arg Ala Asp Met Leu
- 44 20
- 45
- 46 (2) INFORMATION FOR SEQ ID NO: 2:

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/986,682A

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 12 amino acids
49          (B) TYPE: amino acid
50          (D) TOPOLOGY: linear
51      (v) FRAGMENT TYPE: internal fragment
52      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
53      Ser Val Phe Asp Gly Gly Asp Gly Thr Val Tyr Gln
54      1          5          10
55
56      (2) INFORMATION FOR SEQ ID NO: 3:
57          (i) SEQUENCE CHARACTERISTICS:
58              (A) LENGTH: 455 amino acids
59              (B) TYPE: amino acid
60              (D) TOPOLOGY: linear
61          (ii) MOLECULE TYPE: peptide
62          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
63      Met Asn Ser Gly Asp Tyr Lys Glu Asp Tyr Gly Phe Ala His Ile Thr
64      1          5          10          15
65      Arg Ala Asp Met Leu Lys Ile Pro Gly Gln Gln Asn Ser Pro Gln Phe
66      20          25          30
67      Lys Val Pro Gln Phe Asn Ala Ser Ala Ile Lys Asn Ile Asp Ser Ala
68      35          40          45
69      Lys Gly Tyr Asp Lys Ser Gly Asn Leu Ile Asp Leu Asp Val Trp Asp
70      50          55          60
71      Ser Trp Pro Leu Gln Asn Ala Asp Gly Thr Ala Ala Asn Tyr His Gly
72      65          70          75          80
73      Tyr His Ile Val Ser Ala Leu Ala Gly Asp Pro Lys Asn Ser Asp Asp
74      85          90          95
75      Thr Pro Leu His Leu Phe Tyr Gln Lys Val Gly Asp Thr Ser Ile Asp
76      100          105          110
77      Ser Trp Lys Asn Ala Gly Arg Val Phe Glu Asp Met Asp Lys Phe Val
78      115          120          125
79      Pro Asn Asp Pro Tyr Leu Lys Tyr Gln Thr Gln Glu Trp Ser Gly Ser
80      130          135          140
81      Ala Thr Leu Thr Lys Asp Gly Gln Val Arg Leu Phe Tyr Thr Asp Tyr
82      145          150          155          160
83      Ser Gly Asn Pro Glu Asp Gly Gly Thr Gly Ala Gly Asn Gln Ile Ile
84      165          170          175
85      Ser Thr Ala Gln Val Asn Leu Ser Gln Pro Asp Ala Ala Thr Leu Lys
86      180          185          190
87      Val Asp Gly Val Ser Asp His Lys Ser Val Phe Asp Gly Gly Asp Gly
88      195          200          205
89      Thr Val Tyr Gln Asn Ile Gln Gln Phe Ile Asp Glu Gly Lys Trp Ile
90      210          215          220
91      Ser Gly Asp Asn His Thr Leu Arg Asp Pro His Tyr Val Glu Asp Lys
92      225          230          235          240
93      Gly His Lys Tyr Leu Val Phe Glu Ala Asn Thr Gly Thr Thr Asp Gly
94      245          250          255
95      Tyr Gln Gly Asp Gln Ser Phe Asn Asn Lys Ala Tyr Tyr Gly Gly Ser
96      260          265          270
97      Asp Val Phe Phe Gln Asn Glu Lys Asn Lys Leu Leu Gln Ser Pro Lys
98      275          280          285
99      Lys Gln Ile Ala Ser Leu Ala Asn Gly Ala Leu Gly Ile Val Glu Leu

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|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| 100 |     | 290 |     | 295 |     | 300 |     |
| 101 | Ala | Asp | Asp | Tyr | Thr | Val | Lys |
| 102 | 305 |     |     |     |     | 310 |     |
| 103 | Asn | Thr | Val | Ala | Asp | Glu | Val |
| 104 |     |     |     |     |     | 325 |     |
| 105 | Asn | Lys | Trp | Tyr | Leu | Phe | Thr |
| 106 |     |     |     |     |     | 340 |     |
| 107 | Asp | Gly | Ile | Asn | Asp | Lys | Asp |
| 108 |     |     |     |     |     | 355 |     |
| 109 | Ser | Leu | Asn | Gly | Pro | His | Asn |
| 110 |     |     |     |     |     | 370 |     |
| 111 | Asn | Met | Asn | Leu | Asp | Pro | Ala |
| 112 | 385 |     |     |     |     | 390 |     |
| 113 | Gly | Ile | Pro | His | Pro | Glu | Gly |
| 114 |     |     |     |     |     | 405 |     |
| 115 | Thr | Asn | Arg | Gly | Phe | Tyr | Pro |
| 116 |     |     |     |     |     | 420 |     |
| 117 | Leu | Gly | Val | Asn | Ile | Lys | Gly |
| 118 |     |     |     |     |     | 435 |     |
| 119 | Ser | Gly | Gln | Gly | Gln | Phe | Pro |
| 120 |     |     |     |     |     | 450 |     |
| 121 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 129 | ATG | AAC | AGC | GGG | GAC | TAC | AAG | GAA | GAC | TAT | GGT | TTT | GCC | CAT | ATT | ACA | 48  |
| 130 | Met | Asn | Ser | Gly | Asp | Tyr | Lys | Glu | Asp | Tyr | Gly | Phe | Ala | His | Ile | Thr |     |
| 131 | 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| 132 | CGC | GCT | GAC | ATG | CTA | AAA | ATT | CCA | GGA | CAA | CAA | AAC | AGT | CCT | CAA | TTT | 96  |
| 133 | Arg | Ala | Asp | Met | Leu | Lys | Ile | Pro | Gly | Gln | Gln | Asn | Ser | Pro | Gln | Phe |     |
| 134 |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| 135 | AAA | GTG | CCT | CAA | TTC | AAT | GCA | TCA | GCA | ATC | AAA | AAC | ATT | GAT | TCG | GCA | 144 |
| 136 | Lys | Val | Pro | Gln | Phe | Asn | Ala | Ser | Ala | Ile | Lys | Asn | Ile | Asp | Ser | Ala |     |
| 137 |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| 138 | AAA | GGG | TAT | GAT | AAG | TCA | GGC | AAC | TTA | ATA | GAT | TTA | GAT | GTA | TGG | GAT | 192 |
| 139 | Lys | Gly | Tyr | Asp | Lys | Ser | Gly | Asn | Leu | Ile | Asp | Leu | Asp | Val | Trp | Asp |     |
| 140 |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| 141 | AGC | TGG | CCA | CTG | CAA | AAC | GCT | GAT | GGT | ACT | GCG | GCA | AAT | TAT | CAT | GGA | 240 |
| 142 | Ser | Trp | Pro | Leu | Gln | Asn | Ala | Asp | Gly | Thr | Ala | Ala | Asn | Tyr | His | Gly |     |
| 143 |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |     |
| 144 | TAT | CAC | ATC | GTC | TCC | GCT | TTA | GCA | GGT | GAC | CCA | AAA | AAC | AGT | GAT | GAT | 288 |
| 145 | Tyr | His | Ile | Val | Ser | Ala | Leu | Ala | Gly | Asp | Pro | Lys | Asn | Ser | Asp | Asp |     |
| 146 |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| 147 | ACT | CCA | CTT | CAT | TTA | TTC | TAT | CAA | AAA | GTC | GGT | GAT | ACA | TCG | ATT | GAC | 336 |
| 148 | Thr | Pro | Leu | His | Leu | Phe | Tyr | Gln | Lys | Val | Gly | Asp | Thr | Ser | Ile | Asp |     |
| 149 |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     | 115 |     |
| 150 | AGC | TGG | AAA | AAT | GCT | GGA | AGA | GTA | TTT | GAA | GAT | ATG | GAT | AAA | TTT | GTT | 384 |
| 151 | Ser | Trp | Lys | Asn | Ala | Gly | Arg | Val | Phe | Glu | Asp | Met | Asp | Lys | Phe | Val |     |
| 152 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/986,682A

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 153 | CCA | AAT | GAT | CCG | TAT | CTT | AAA | TAT | CAA | ACA | CAG | GAG | TGG | TCA | GGT | TCT | 432  |
| 154 | Pro | Asn | Asp | Pro | Tyr | Leu | Lys | Tyr | Gln | Thr | Gln | Glu | Trp | Ser | Gly | Ser |      |
| 155 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |     | 145 |      |
| 156 | GCT | ACT | TTA | ACC | AAA | GAT | GGC | CAA | GTC | CGT | TTA | TTC | TAT | ACA | GAT | TAC | 480  |
| 157 | Ala | Thr | Leu | Thr | Lys | Asp | Gly | Gln | Val | Arg | Leu | Phe | Tyr | Thr | Asp | Tyr |      |
| 158 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     | 160 |      |
| 159 | TCA | GGT | AAT | CCT | GAA | GAT | GGT | GGA | ACC | GGT | GCT | GGT | AAC | CAA | ATC | ATT | 528  |
| 160 | Ser | Gly | Asn | Pro | Glu | Asp | Gly | Gly | Thr | Gly | Ala | Gly | Asn | Gln | Ile | Ile |      |
| 161 |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     | 175 |      |
| 162 | TCA | ACT | GCT | CAA | GTA | AAC | TTA | TCC | CAG | CCG | GAT | GCA | GCT | ACA | CTT | AAA | 576  |
| 163 | Ser | Thr | Ala | Gln | Val | Asn | Leu | Ser | Gln | Pro | Asp | Ala | Ala | Thr | Leu | Lys |      |
| 164 |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     | 195 |      |
| 165 | GTC | GAT | GGA | GTA | TCT | GAT | CAT | AAA | TCT | GTC | TTT | GAT | GGC | GGA | GAC | GGT | 624  |
| 166 | Val | Asp | Gly | Val | Ser | Asp | His | Lys | Ser | Val | Phe | Asp | Gly | Gly | Asp | Gly |      |
| 167 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     | 210 |      |
| 168 | ACA | GTT | TAT | CAA | AAT | ATT | CAG | CAA | TTT | ATC | GAT | GAA | GGC | AAG | TGG | ATT | 672  |
| 169 | Thr | Val | Tyr | Gln | Asn | Ile | Gln | Gln | Phe | Ile | Asp | Glu | Gly | Lys | Trp | Ile |      |
| 170 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |     | 225 |      |
| 171 | TCA | GGT | GAT | AAC | CAT | ACT | TTA | AGA | GAC | CCT | CAC | TAT | GTT | GAA | GAT | AAG | 720  |
| 172 | Ser | Gly | Asp | Asn | His | Thr | Leu | Arg | Asp | Pro | His | Tyr | Val | Glu | Asp | Lys |      |
| 173 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |     | 240 |      |
| 174 | GGC | CAT | AAA | TAT | CTT | GTC | TTT | GAA | GCG | AAT | ACT | GGA | ACA | ACA | GAT | GGT | 768  |
| 175 | Gly | His | Lys | Tyr | Leu | Val | Phe | Glu | Ala | Asn | Thr | Gly | Thr | Thr | Asp | Gly |      |
| 176 |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     | 255 |      |
| 177 | TAT | CAA | GGC | GAT | CAG | TCT | TTT | AAT | AAT | AAA | GCT | TAC | TAT | GGC | GGA | AGT | 816  |
| 178 | Tyr | Gln | Gly | Asp | Gln | Ser | Phe | Asn | Asn | Lys | Ala | Tyr | Tyr | Gly | Gly | Ser |      |
| 179 |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |     | 275 |      |
| 180 | GAC | GTC | TTC | TTC | CAG | AAT | GAA | AAA | AAT | AAA | CTG | CTT | CAA | AGT | CCT | AAA | 864  |
| 181 | Asp | Val | Phe | Phe | Gln | Asn | Glu | Lys | Asn | Lys | Leu | Leu | Gln | Ser | Pro | Lys |      |
| 182 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |     | 290 |      |
| 183 | AAA | CAA | ATT | GCT | TCT | TTA | GCG | AAT | GGT | GCA | TTA | GGC | ATT | GTT | GAA | TTG | 912  |
| 184 | Lys | Gln | Ile | Ala | Ser | Leu | Ala | Asn | Gly | Ala | Leu | Gly | Ile | Val | Glu | Leu |      |
| 185 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |     | 305 |      |
| 186 | GCC | GAT | GAC | TAT | ACA | GTG | AAA | AGT | GTT | ATG | AAA | CCA | TTA | GTC | GCA | TCA | 960  |
| 187 | Ala | Asp | Asp | Tyr | Thr | Val | Lys | Ser | Val | Met | Lys | Pro | Leu | Val | Ala | Ser |      |
| 188 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |     | 320 |      |
| 189 | AAC | ACA | GTA | GCA | GAT | GAA | GTC | GAA | CGC | GCC | AAT | ATA | TTT | AAA | ATG | AAT | 1008 |
| 190 | Asn | Thr | Val | Ala | Asp | Glu | Val | Glu | Arg | Ala | Asn | Ile | Phe | Lys | Met | Asn |      |
| 191 |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     | 335 |      |
| 192 | AAT | AAA | TGG | TAT | CTA | TTC | ACG | GAT | TCA | AGA | GGA | TCC | AAA | ATG | ACG | AGT | 1056 |
| 193 | Asn | Lys | Trp | Tyr | Leu | Phe | Thr | Asp | Ser | Arg | Gly | Ser | Lys | Met | Thr | Ser |      |
| 194 |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     |     | 355 |      |
| 195 | GAT | GGA | ATT | AAC | GAC | AAA | GAT | GTT | TAT | ATG | CTA | GGG | CCC | GGA | GGC | GAC | 1104 |
| 196 | Asp | Gly | Ile | Asn | Asp | Lys | Asp | Val | Tyr | Met | Leu | Gly | Pro | Gly | Gly | Asp |      |
| 197 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |     | 370 |      |
| 198 | TCC | TTA | AAT | GGC | CCA | CAC | AAC | CCG | ATA | AAT | GAA | ACT | GGA | CTT | GTA | TTG | 1152 |
| 199 | Ser | Leu | Asn | Gly | Pro | His | Asn | Pro | Ile | Asn | Glu | Thr | Gly | Leu | Val | Leu |      |
| 200 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |     | 385 |      |
| 201 | AAC | ATG | AAT | CTT | GAC | CCT | GCT | GAT | CTC | ACA | CAC | ACT | TAC | TCT | CAT | TGC | 1200 |
| 202 | Asn | Met | Asn | Leu | Asp | Pro | Ala | Asp | Leu | Thr | His | Thr | Tyr | Ser | His | Cys |      |
| 203 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     |     |     | 400 |      |
| 204 | GGT | ATC | CCG | CAC | CCT | GAA | GGT | AAT | AAT | GTG | GTA | CTC | ACA | AGT | TAT | ATG | 1248 |
| 205 | Gly | Ile | Pro | His | Pro | Glu | Gly | Asn | Asn | Val | Val | Leu | Thr | Ser | Tyr | Met |      |

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/986,682A

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206          405          410          415
207 ACG AAT AGA GGC TTC TAT CCA GAA CAT CAC TCT CAC CTG CGG GAC AAG 1296
208 Thr Asn Arg Gly Phe Tyr Pro Glu His His Ser His Leu Arg Asp Lys
209 420          425          430          435
210 CTT GGG GTT AAT ATT AAA GGG TCT GAC ACA TCT GGA GGA GAA AAT AGT 1344
211 Leu Gly Val Asn Ile Lys Gly Ser Asp Thr Ser Gly Gly Glu Asn Ser
212          440          445          450
213 TCC GGA CAA GGA CAA TTC CCA 1365
214 Ser Gly Gln Gly Gln Phe Pro
215          455
216
217 (2) INFORMATION FOR SEQ ID NO: 5:
218 (i) SEQUENCE CHARACTERISTICS:
219 (A) LENGTH: 2408 base pairs
220 (B) TYPE: nucleic acid
221 (C) STRANDEDNESS: double
222 (D) TOPOLOGY: linear
223 (ii) MOLECULE TYPE: genomic DNA
224 (vi) ORIGINAL SOURCE:
225 (A) ORGANISM: Bacillus sp.
226 (C) INDIVIDUAL ISOLATE: V230 (FERM BP-5054)
227 (ix) FEATURE:
228 (A) NAME/KEY: signal peptide
229 (B) LOCATION: 1..360
230 (C) IDENTIFICATION METHOD: E
231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
232 CGGGGAAAAT ACTAGATTCC AATTGGCCAG ACTTCCCAGT TGGTGTAAGA GAAGAGTTTCG 60
233 GACTGCCAAT GCAGCTGTGC GTAAGAAAAC AGCTTACTCA TGAGCAATTA CTAGAAGAAT 120
234 TTCAAAGTC CTGGGATAAG GCCAAGTCCA CTTTGAAATA AACTTTTCAG CCTCTGTGTG 180
235 GGGGCTTTTT TGTTTTTTATT TATTTCAACT GCAAGTGGTC CATCCCCTAT ATCAATTTAA 240
236 GACGAAATTC TAATCAATCC ATGCCATCCC CAATAAACTC GTCCTCCTCT ATACTTTTAA 300
237 TTAATAAGAA ACTATCAAGA GCTTTCCTAT CAAATTCATA CATATCCAAG GAGGGAGACG 360
238 ATG AAC TTC AAA AGA TTG GCG AAA AAA GCA GCT GCC GTA ACC TTC AGG 408
239 Met Asn Phe Lys Arg Leu Ala Lys Lys Ala Ala Val Thr Phe Arg
240 -30 -25 -20
241 ACT GCT ATA TTA GTA GGA GCG GAC GGA CCG CAT ATT TTT GCG CAG CAA 456
242 Thr Ala Ile Leu Val Gly Ala Asp Gly Pro His Ile Phe Ala Gln Gln
243 -15 -10 -5
244 ATG AAC AGC GGG GAC TAC AAG GAA GAC TAT GGT TTT GCC CAT ATT ACA 504
245 Met Asn Ser Gly Asp Tyr Lys Glu Asp Tyr Gly Phe Ala His Ile Thr
246 1 5 10 15
247 CGC GCT GAC ATG CTA AAA ATT CCA GGA CAA CAA AAC AGT CCT CAA TTT 552
248 Arg Ala Asp Met Leu Lys Ile Pro Gly Gln Gln Asn Ser Pro Gln Phe
249 20 25 30
250 AAA GTG CCT CAA TTC AAT GCA TCA GCA ATC AAA AAC ATT GAT TCG GCA 600
251 Lys Val Pro Gln Phe Asn Ala Ser Ala Ile Lys Asn Ile Asp Ser Ala
252 35 40 45
253 AAA GGG TAT GAT AAG TCA GGC AAC TTA ATA GAT TTA GAT GTA TGG GAT 648
254 Lys Gly Tyr Asp Lys Ser Gly Asn Leu Ile Asp Leu Asp Val Trp Asp
255 50 55 60
256 AGC TGG CCA CTG CAA AAC GCT GAT GGT ACT GCG GCA AAT TAT CAT GGA 696
257 Ser Trp Pro Leu Gln Asn Ala Asp Gly Thr Ala Ala Asn Tyr His Gly
258 65 70 75 80

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/986,682A**

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Line

Error

Original Text

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**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/09/986,682A**

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*INPUT SET: S36770.raw*

< < THERE ARE NO ITEMS MISSING > >

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**SEQUENCE CORRECTION REPORT**  
**PATENT APPLICATION US/09/986,682A**

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*INPUT SET: S36770.raw*

| Line | Original Text                               | Corrected Text                              |
|------|---|---|
| 226  | (C) INDIVIDUAL ISOLATE: V230 (FERM BP-5054) | (C) INDIVIDUAL ISOLATE: V230 (FERM BP-5054) |